

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

>*CtManS* -1964 bp.

GGAATTGGCACGAGGTGCCTGCAACAAGTCACTAGTCCATCCTGCAGTCCCTAACCCCT
CCCTAGTGTCTTCTTCAGGCTCCATATTCCCTTATAACTACTACAATAGATACAATG
AGAAACCTAATCTCGAGGAGCCTGAAGGGATTCCAGGCAACAGTCAAGCAGTCTGCGC
TATGCCCTGGCAATCAATTCTGCCCCAGTGATCATACCTCTTCTAAAACCTAGCAGTCATA
GTGTGCTCAGTTATGTCATCATGCTATTGTTGAAAGAGTAGCCATGGCAGCTGTAATT
TTGATTGTCAAAGTGTGAGGAAGAAAAGATAACCCAAGTATAACTTGGAAAGCCATGAAA
CAGAAGCTAGAGAGAAGCAAAAATACCCATGGTCTGATCCAATACCTATGTATAAC
GAGAAAGAGGTGTACAAGCTTCCATTGGAGCAGTATGTTGGCTTCATGGCCAGCTGAC
AGGTTCATAGTTCAAGTTCTGATGACTCAACAAATCCAGTCTTAAGGGAGTTGGTTGAA
ATGGAGTGTCAAAAATGGATAACAGAAAGGTGTGAATGTCAAGTATGAAAATAGGAGAAAAT
CGCAATGGTTACAAAGCAGGTGCTTAAAGAGGGTTGGAGAAGCAATATGTAGAGGAT
TGTGAGTTTAGCAATATTGATGCAAGATTCCAACCAGATGCGGATTTCTTGGAAC
ACAATTCCCTATCTGCTGGAAAATCCAAGTTGGTTGGTCAAGGCGAGATGGAAATT
GTGAACTCAGAAGAATGTATGATGACACGGCTCAAGAGATGTCACTAGATTACCACTT
AGTGTGAACAGGAAGTGGCTTCAACATACTCATTCTCGGTTCAATGGAACAGCA
GGAGTTGGCGGATCCAAGCCATAAAAGATGCTGGAGGATGAAAAGACCGAACACGGTG
GAGGATATGGACCTTGCAGTTAGAGCAAGCTTGCATGGCTGGAAATTGTTTGTGGGT
GATGTAAGGTCAAAAATGAATTACCAAGTACATTAAAGCATATCGATTTCAGCAGCAC
AGGTGGTCATGCGGTCAGCTAATCTCTTAAAGAAATGACCAAGGAAATCATCTGTTGC
AAAAGGGTGCCACTCTCAAGAGACTCCATCTCATCTATGCTTCTTGTGAGAAAAA
ATAGTTGCACACTGGTTACGTTCTTCTTACTGCATAGTTACCAAGCTTGTGATA
GTTCCCAGGTTAACATCTCAAAAGCAGATTGCCATATACATCCCAGCAACCATTACAATT
CTAAATGCAGTCTCCACCCCAAGATCCATGCATCTACTAGTACTCTGGATACTCTTGAG
AATGTCATGTCACTCCATCGAACTAAAGCAGCAATTATTGGACTCTTGGAAAGCAAATCGT
GTCATGAATGGGTTGTGACTGAGAAGCTTGGAAATGCCATGAAACAGAGGAACAATGCT
AGGCCATCAAGAGCTTACGGTTCGAATTATAGAAAGGATCCACCCATTGGAGATTATA
GTGGGGATGTATATGCTGCACTGCAACCTATGACCTGTTATTGGACACGACCATTTC
TTTGTCTATCTCTGTTGCAGGCAGGGCGTTCTTACAATGGGATTGGCCTAGTAGGA
ACAATTGTACCCACCTAAAGCTTAAAGGTCACTGGACTCATGAAACATAAGTATTAGTGTAT
GAACGGGTCTGTTGTTAAAGACTCTAAGTCTAGTGAACTAGCTATCCATAAGCATAAG
AACTGTAAGAGAAGCTACGGCTACTTAGTAGAAGCATTCCATATGGTATCAGGACTTCTT
TGTACCCATGTATAAGAACCGAGAATCAAACGTATAAACATGTCCATAATATGAAGCTTA
AATAAATCTGTTATCTGCACTAAAAAAAAAAAAAAAC

FIGURE 1

>CtMANS - 526 aa.

MRNLIFEPEGIPGNSSSSLRYAWQSIRAPVIIPLLKLAVIVCSVMSIMLFVERVAMAAV
ILIVKVLRKRYTKYNLEAMKQKLERSKKYPMVLIQIPMYNEKEVYKLSIGAVCGLSWPA
DRFIVQVLDDSTNPVLRELVEMECQKWIQKGVNVKYENRRNRNGYKAGALKEGLEKQYVE
DCEFVAIFDADFQPDADFLWNTIPYLLENPKLGLVQARWKFVNSEECMMTRLQEMSLDYH
FSVEQEVSSTYSFFGFNGTAGVWRIQAIKDAGGWKDRTTVEDMDLAVRASLHGWEFFV
GDVKVKNELPSTFKAYRFQQHRWSCGPANLFKKMTKEIICCKRVPLLKRLHLIYAFFFVR
KIVAHWVTFFFYCIVIPACVIVPEVNLKKQIAIYIPATITILNAVSTPRSMHLLVLWILF
ENVMSLHRTKAAIGLLEANRVNEWVVTEKLGNAMEKQRNNARPSRASRFRIIERIHPLEI
IVGMYMLHCATYDLLFGHDFFVYLLLQAGAFFTMGFLVGTIVPT

FIGURE 2

>*CtGa/T2* - 1609 bp.

GGAATTCCGCACGAGGCTCCCATGGCAAATCCTCCAATTCCAGAAACAAAATTCACAC
GTAAACCTCTCCGACGGTTCTCTTCTCGCCGGAGCATTCTCCCGCTTCTAATCGTT
TGGGGTTCTCCTCCTCACACCCCCATCCCTAACGAAACCCAACCTTCGAATCACTT
TCGGTAAATTCTCACCAAAACGACGCCGTTCGCGGGGGACCGGATTCCGGTTCGAT
CCCCCGGACCGGACTTCTACGACGACCCGGAAATGGGGTACACCATAGACACGACGGTG
CGAGATTGGGATGCAAAGCGTGGAGGAGTGGCTGGCGCTTCATCCTCCTCGCCGCCGA
GCGAGAGAACGAGTTGGTGGTACCGGATCGCAGCCGGCACCGTGCCGAATCCCATC
GGCAGCACTTGTGTTACGGTTTAAGAACAAAGGTGGATTACTGTCGGTTACACGGG
TACGATATCGTGTACAACAATGCATTGTTACACCCGAAATGTTACGTATTGGGCGAAG
TACCCGGTGGTGCAGGGCGCGATGATGGCCACCCGGAAAGCCGAGTGGATCTGGTGGTC
GACTCGGACCGTTGTTACCGACATGGAGTTCAAACCTACCAATTAGATCACTACAAGGAT
CACAAACCTCGTCGTCATGGCTGGGCCACCTCATCCACGAGAAACGTAGTGGACGGC
CTCAACGCCGGCGTCTCCTCATCAGAAACTGTCAATGGTCAATTGGACTTCATAAACGAA
TGGGCCAGCATGGGCCACAAACTCCGAACTACGAGAAATGGGTCAAACCTAAAGTCA
ACTTTCAAAGACAAATTCTCCGGAGTCAGACGATCAGACGGCCTCGCTTACCTGATC
GCGATCGAGAAAGAAAAATGGCGGACAAGATTACTTAGAGAAACTCGTATTATTCGAA
GGGTACTGGGAAGAAATCGTCCAACATTGAGAATATAAGCAAGAAATACAACGAGATC
GAAACGGGGGTGCGCAGGTTAAGAACGGCAGCAGGGAGAAAGTGAAGCTTACGGT
GAAGAGAGGGAGAAATTTAACGGAAGCAGGTAACGGTAAAGGAAGCTGGAGACGGCG
TTTGTGACGCACTTCACGGGGTGTCAACCTGTAGCGGAAATATAACGCTATGTATAAC
GCCGAAGATTGTTGGAACGGAATCGTAAAGCCCTTAATTGCTGATAATCAGGTGATG
CGTAAATATGGTTCTGTACACCCGGATGTACTAGATAATTCCGTTGCGGATTCCGTTT
GATTATCCCCCTAACCGCTCAGGTAATAATCATATTAAATGGAATCTAATTATTGTTGAC
CGCTGGCTACTCAGATTCTCATGTGTTCTGAAAGTACTAGTACTAGTATTAAATT
TCTTAGTGTATATTATAATATTGATATTCTGGCTTTGCATATAATAGT
ATCGTGTGGAGTAGTATTAAATTATGCATAAGTGAAGGGATAATTATCTTTCGAAT
CCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACT

FIGURE 3

>CtGALT2 - 445 aa.

MAKSSNSRNKISHVNLSDGFLFLAGAFSAFLIVWGFSSTTPIPNETPTFESLSVNSHQND
DAVSRGGPDFRFDPPDRTFYDDPEMGTIDTTVRDWDAKREEWRLHPSFAAGARERVLV
VTGSQAPCRNPIGDHLLRFFKNKVDYCRLHGYDIVYNNALLHPKMFTYWAKYPVVRAA
MMAHPEAEWIWWVDSDALFTDMEVXLPLDHYKDHNLVVGWAHLIHEKRSWTGLNAGVFL
IRNCQWSLDFINEWASMGPQTPNYEKWGQTLKSTFKDKFFPESDDQTGLAYLIAIEKEKW
ADKIYLENSYYFEGYWEEIVGTFENISKKYNEIETGVRLRRRAEKVSEAYGEEREKYL
TEAGNGKGWSRRPFVTHFTGCQPCSGKYNAMYNAEDCWNGMRKALNFADNQVMRKYGFVH
PDVLDNSVSPIPFDYPRNRSGNNHI

FIGURE 4

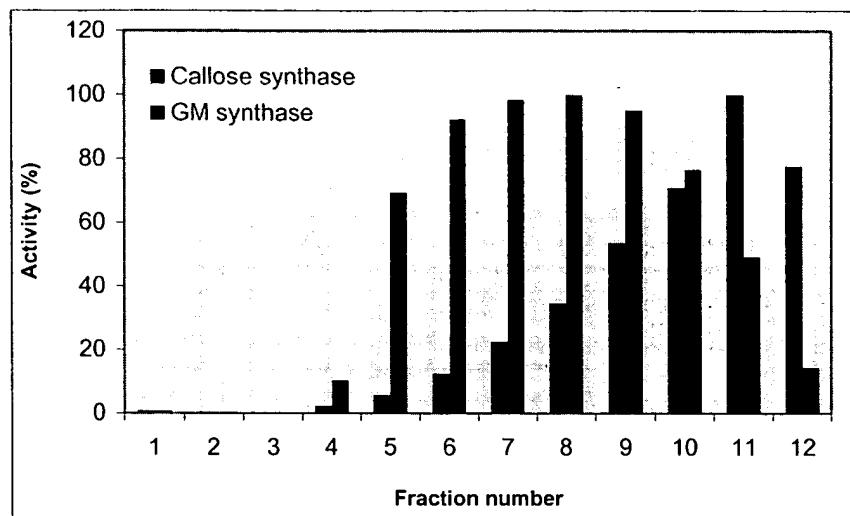


FIGURE 5

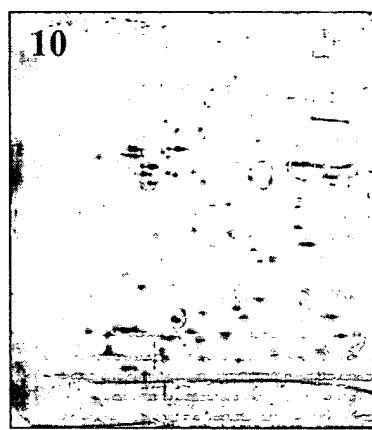
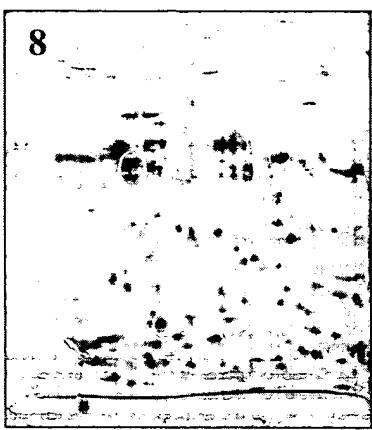
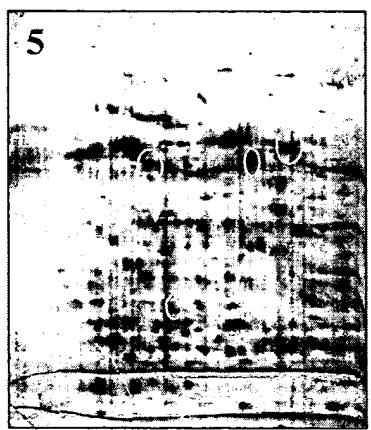


FIGURE 6

	1	60
Fenugreek	(1)	----- GCGACGAAATTGG
Guar-Galt1	(1)	GGAATTGGCACGAGGCTCCAGTATCAATTCACTCACTCCCATGGCAAATTGG
Guar-Galt2	(1)	----- GGAATTGGCACGAGGCTCCCATGGCAAATTCCCAAAT
Consensus	(1)	----- G A C CTCCCATGGCGAAATTGG
	61	120
Fenugreek	(16)	TCCAAAACAAATCCTCTCC-----ATGGCTCTCAAAATGGTGCATCTTCCTCTAGGTGCA
Guar-Galt1	(58)	TCCAGAAACAAATCCTCTAA-----ATGGATCTCCAACGGTTGCTGCTTCCTCTAGGAGCA
Guar-Galt2	(40)	TCCAGAAACAAATTCACACGTAACCTCTCGACGGTTGCTTCCTCGCCGAGCA
Consensus	(61)	TCCAGAAACAAATCCTCTCA ATGGCTCTCCAACGGTTGC TCTTCCTCTAGGAGCA
	121	180
Fenugreek	(73)	ATGTCAGCTCTTCTTATGATTGGGGGCTCAATTCCTTCATCGCTCCAAATCCAAAATCC
Guar-Galt1	(115)	TTCACTGCTCTTCTCTGCTGGGTTTATGCTCCCTCATCCATCCCCATCCAAAACACC
Guar-Galt2	(100)	TTCTCGCGCTTCTAACTGTTGGGTTCTCTCCCTCAACCCCCATCCCTAACGAA
Consensus	(121)	TTCTC GCTCTTCTTATG TTTGGGTTCTCTCCCTCATCACCCCCATCCAAAAC CC
	181	240
Fenugreek	(133)	AACCCAAAATTCAACTCCCTCACCAACCAAACCTCAAATCTTAAACCTTCACCAACACCC
Guar-Galt1	(175)	GACCCCGAGCTCAACTCCGCGCCACCGATTTGGAGATCCCTAACCTTCCAAAACCC
Guar-Galt2	(160)	AACCCAAACCTTCGTAACGAT-----T-----TCCGTTAACCTAACGAA
Consensus	(181)	AACCCAAA TTCAACTCC TC CCACCA T T A ATCC TAAACTTCCAAAAC CC
	241	300
Fenugreek	(193)	A-----AG-----TTGGCTGGTCTGATTTGTTACATGACCCCTGAGACAAAACCTTCTATGAT
Guar-Galt1	(235)	GCTGCCAC-CTTGCC-----TCCCACTTGCACACGACCCCTCGTACACCCACCTTCTACGAC
Guar-Galt2	(205)	GGCGTTTGGCGGGGGACGGGATTTCCGTTGATCCCCCGACCGGACTTTCTACGAC
Consensus	(241)	GC G AC CTTGC GGTCC GATTGC GCACGACCCCTCC GACA ACCTTCTACGAC
	301	360
Fenugreek	(247)	GATCCAGAAAATGTTACACCATGATGGACAAACCAATGAAAAATTGGGATGAGAAGCGT
Guar-Galt1	(292)	GACCCCGAAACCAAGCTTACCAT-----GGACAAACCAATGAAAACCTGGAGAGAGCGT
Guar-Galt2	(265)	GACCCCGAAATGGCTACACCAT-----AGACGAGCTGCGACATTGGGATGCAAGCGT
Consensus	(301)	GACCC GAAAC GTTACACCAT GGACAAACCAATGAAAAATTGGGATGAGAAGCGT
	361	420
Fenugreek	(307)	AAAGAAATGGCTATTCATCATCCTCATTCGCGCTGGAGCAACCGAAAAGATACTTGTT
Guar-Galt1	(349)	AAGGAGTGGCTGGCTGCATCATCTCGTTGGCGCCAGCAGCGATAAGATTCTCC TG
Guar-Galt2	(322)	GAGGAGTGGCTGGCTGCCTCATCCCTCCCTCGCCGGAGGAGAGAACGAGTTTGCTG
Consensus	(361)	AAGGAGTGGCTGCTGCATCATCCTC TTGGCCGGAGCAAGCGAAAAGATTCT GTG
	421	480
Fenugreek	(367)	ATAACGGGTCAACAGCGACAAAGTGTGCAACCCATCGGAGACCCACCTTACTAAGG
Guar-Galt1	(409)	GTGACAGGTTCTCAGCGAACCGGTGCCATAACCGATCGGGACCCACCTCTGGCG
Guar-Galt2	(382)	GTGACCGGATCGTAGCGCCACCGTGCCTGGATCCCATCGGGACCAACTGGTGTACGG
Consensus	(421)	GTGAC GGTTC CAGCGACAC GTGCCA AACCCATCGGCACCCACCT CTGTTACGG
	481	540
Fenugreek	(427)	TTCTATAAAAACAAGGTGATTATGTCGATAACACAACCGACATAACTACAAACAAT
Guar-Galt1	(469)	TTTTTCAGAACAAAGGTGGATTACTGCGGGCTGACAAACTACGACATAAT TACAAACAAC
Guar-Galt2	(442)	TTTTTTAAAGAACAAAGGTGGATTACTGCGGTTACACGGGTACCGATACTGTTACAAACAAT
Consensus	(481)	TTTTTTAAAGAACAAAGGTGGATTACTGCGG TACACAACGACATAAT TACAACAAT
	541	600
Fenugreek	(487)	GCATTGGTGCACCCAAAATGGACTCTTACTGGCCAAGTATCTATGGTTCGGCGGA
Guar-Galt1	(529)	GCGCTTCTGCTCATCTAAAATGAACCTCTTATGGGCCAAGTATCCAGTGATTGGCG
Guar-Galt2	(502)	GCATTGGTACACCCGAAAATGTTACGTTATGGCGAAGTACCGGTGGTGCGGGCCCG
Consensus	(541)	GCATTGGTGCACCC AAAATG ACTCTTATGGCCAAGTATCC GTGGTTCGGCCCG
	601	660
Fenugreek	(547)	ATGTTGGCCCATCCGGAAGTGAATGGATATGGTGGGTGCACTCTGATGCCAATCTTACG
Guar-Galt1	(589)	ATGATGGCCCATCCGGAAGTGGAGTGGCTGGTGGGTGGACTCGGACGCCGTTTCACG
Guar-Galt2	(562)	ATGATGGCCCATCCGGAAGCCTGGAGTGGATCTGGTGGGTGCACTCGGACGCCGTTTCACG
Consensus	(601)	ATGATGGCCCATCCGGAAGT GAGTGGAT TGGTGGGTGCACTCGGACGCCG T TTCAAC
	661	720
Fenugreek	(607)	GATATGAAATTCAACTTACCGTTATGGCGTTAACAGGATCACAACTTGTGATTCATGGT
Guar-Galt1	(649)	GACATGGAGTTCAAGCTTCCGTTAACAGGTTATAGAACCCACAAATCTGGTGGTTACGGT
Guar-Galt2	(622)	GACATGGAGTTCAACTACCAATTAGATCACTACAGGATCACAAACCTCGTCGTCCATGGC
Consensus	(661)	GACATGGAGTTCAAGCTACCGTTA AGCGTTACAAGGATCACAAACCT GTGGTTCATGGT

FIGURE 7a (Sheet 1 of 3)

		721	
Fenugreek	(667)	TGGGAAGAGTTGGTTAAGACAGAGCATAGTGGACCGGGCTAACGCGGGTGTTTCTTG	780
Guar-Galt1	(709)	TGGGAAGGATTGGTACGGTTAACCATAGCTGGACGGGTCTAACGCGGGCTATTCTTG	
Guar-Galt2	(682)	TGGCCACCTCATCAGAGAAACGTAGTTGGACGGGCTAACGCGGGTCTCTC	
Consensus	(721)	TGGGAAGA TTGGT CAG GAA CATAGTTGGACGGG CT AACGCGGGCGT TTCTTG	
	781		840
Fenugreek	(727)	ATGAGGAATTGTCAATGGTCGTTGGATTTATGGATGTTGGCCAGTATGGGCCAAC	
Guar-Galt1	(769)	ATTCGGAATTGCCAGTGGTCGTTGGAGTTCATGGATGCTGGGTGAGCATGGGCCACAG	
Guar-Galt2	(742)	ATCAGAAACTGTCAATGGTCATGGACATTCAATACGAATGGCCAGCATGGGCCACAA	
Consensus	(781)	AT AGGAATTGTCAATGGTCGTTGGA TTCAATGGATGT TGCCCCAGCATGGGCCACAA	
	841		900
Fenugreek	(787)	AGC CCGGAATACGAGAAATGGGGGAGAGACTTAGAGAAACTTTAACAGACAAAGTCGT	
Guar-Galt1	(829)	ACTCCGAATACGAGAAATGGGGGAGAGCTGGAGAGAGACTCAAGGACAAAGTCGTG	
Guar-Galt2	(802)	ACTCCGAATACGAGAAATGGGGTCAACCTAACAGTCAGTCAACTTTAACAGACAAATCTC	
Consensus	(841)	ACTCCGAATACGAGAAATGGGGGAGAG CT AGAGAAACTTCAAGGACAAAGTG T	
	901		960
Fenugreek	(847)	CGTGATTCAAGATGATCAGACGGCGCTGCTTACTTGTATCGCGATGGGAGA	
Guar-Galt1	(889)	CCTGATTGCGACGATCAGACGGCGCTGCTTACCTGTATCGCGACGGATAATAAGGACACG	
Guar-Galt2	(862)	CCGGAGTCAGACGATCAGACGGCGCTGCTTACCTGTATCGCGATCGAGA	
Consensus	(901)	CCTGATTCAAGACGATCAGACGGCGCT GCTTACCTGTATCGCGATGGGA AA GGACAAG	
	961		1020
Fenugreek	(904)	TGGACAAAGAGATCTATAAGGAGAACTGACTTATTGTAAGGGTATGGTTAGAGAT	
Guar-Galt1	(949)	TGGAGGGAGAAGATCTCTTGGAGAGCGAGTACTACCTTCGAAGGGTACTGGCTGGAGATC	
Guar-Galt2	(919)	TGGGGGAGAAGATTTACTTAAAGAAACTCGTATTATTCGAAGGGTACTGGGAAGAAATC	
Consensus	(961)	TGGACGGAGAAGATCTACTTGGAGAACGAGTATTATTCGAAGGGTACTGG TAGAGATC	
	1021		1080
Fenugreek	(964)	TCAAAGATGTATGATAAAATGGGTGAGAGATATGATGAGATAAGAAAAGAGTGGAAAGGG	
Guar-Galt1	(1009)	GTGAAGACGTACGAGAACTAACGGGAGGCTATGATGAGGCTGGAGGAAGGTGGAAGGG	
Guar-Galt2	(979)	CTCGGAACATTCGAGATAAAAGCAACATACAGATGAAACGGGCTGCGCAGG	
Consensus	(1021)	GT AAGACGTACGAGAA ATAAGCGAGAGATATGATGAGAT GAAA GAGGGTGGAAAGGG	
	1081		1140
Fenugreek	(1024)	TTAACGGAGGAGGCATGCAGAGAAAGTCAGTGAACTGTTATEGTGAAATGAGAACAGGAGTAT	
Guar-Galt1	(1069)	TTGAGGAGGAGGCATGGGAAAGTCAGCGAGAAATACGGTCGATGAGGGAGGAGTAT	
Guar-Galt2	(1039)	TTAAGGAAGGCTCACGGGAGAAAGTGAGTGAGCTTACGGTAAAGAGAGGGAGAAATAT	
Consensus	(1081)	TTAAGGAGGAGGCATGGGAGAAAGTGAGTGAA TTACGGTAAATGAGGGAGGAGTAT	
	1141		1200
Fenugreek	(1084)	CTTAAGAATTAGGGATAT-----GAGAACACCTTTTATTAACATTTTACA	
Guar-Galt1	(1129)	CTGAAGGACA-----ACAA-----GAGGAGGCCCTTTATCACCGCACTTTACT	
Guar-Galt2	(1099)	TTAACCGAACCGAGTAACGGTAAAGGAAGCTGGAGACGGCCCTTGTGACGCACCTTCACG	
Consensus	(1141)	TAAGGA AGG ACA GAGAACGCC TTTATACGCACCTTTAC	
	1201		1260
Fenugreek	(1132)	GGGTGCAACCTTGTAAATGGTCATCATATAATGCTGGAGATGATTGCTGGAAAT	
Guar-Galt1	(1171)	GGGTGTCACCCCTGTAAATGGCCACCATAACTCTGCTTATAATGGTAATGATTGCTGGAAAT	
Guar-Galt2	(1159)	GGGTGTCACCTTGTGCGEAAATATAACGGCTATGATAACCGGAAAGATCTGGAAAC	
Consensus	(1201)	GGGTGTCACCTTGTAAATGG CA CATAATCCTAT TATAATGC GATGATTGCTGGAAAT	
	1261		1320
Fenugreek	(1192)	GGCATGGAGAGAGCTCTAACATTGCTGATAATCAGGTGTTGGCGAACGTTGGTTTCATT	
Guar-Galt1	(1231)	GGCATGGAGAGGGCTTAAATTCGCTGATAATCCTGGCTACTTACGGTTATCAC	
Guar-Galt2	(1219)	GGATGGCTAACGCCCTAAATTCGCTGATAATCAGGTGATGGCTAAATGGTTTCGTAA	
Consensus	(1261)	GGCATGGAGAGAGCTTAAATTCGCTGATAATCAGGTGTTGGCGTAA TATGGTTTC T	
	1321		1380
Fenugreek	(1252)	CATCCAAATCTATGGATAAGTCTGTTCTCCTAACATTACCAATTGGATA-----CCCGCTGCATC	
Guar-Galt1	(1291)	CGTCAAAATTTACTCGAACAGTCTGTTCACTCTACCTTTGGTAA-----CCGTCTGCATA	
Guar-Galt2	(1279)	CACCCGGATCTACTACATAATTCGTTTGCCTGAATTCGGTTGATATTCCCGTAAACCGG	
Consensus	(1321)	CATCCAAAT TACT GATAAGTCTGTTTC CC TTACCTGGTTA CCCCGCTGCATC	
	1381		1440
Fenugreek	(1311)	ACCATAATA-TATTTATAACCTGAGGGTA-AATTATAATAG-TAATTGTTATGATGA	
Guar-Galt1	(1350)	-----TAATG-TACTACTAC-TG-----ATAACGACAG-ATATT-TAAATTTA	
Guar-Galt2	(1339)	TCAGGTAAATAATCATATAATGAAATCTAATTATGTTGACGCCCTGGCTACTCAGATTC	
Consensus	(1381)	AC TAATA TA TATTAC TG A A AAT ATGACAG T ATT TAAAGATTA	
	1441		1500
Fenugreek	(1367)	TTCTTCTGTCATAAATTAATCAAAATAATGAAGGTGGTGTGATGATATTAGC-----	
Guar-Galt1	(1391)	TTATAC-GAAAAA-----AATCAAAATAATCAAAATAATCAAAATAATCAAAATAATCA	
Guar-Galt2	(1399)	TCGATGTTCTGTAAGTACTCTGACTACTAGTATTAATTCCTAGTGTATATTTAT	
Consensus	(1441)	TTCTTCTGT AA AAAAATAAAATAAT GT T A T TTAG	

FIGURE 7b (Sheet 2 of 3)

	1501	1560
Fenugreek	(1416)	-----
Guar-GaLT1	(1418)	-----
Guar-GaLT2	(1459)	AATATTTTATTGTATTTCTGGCGTTGCATATAGTATCGTGTGGAGTAGTATT
Consensus	(1501)	
	1561	1620
Fenugreek	(1416)	-----
Guar-GaLT1	(1418)	-----
Guar-GaLT2	(1519)	TAATTATGCATAAGTGAAGGGATAATTTATTCTTTCGAATCCCTAAAAAAAAAAAAAA
Consensus	(1561)	
	1621	1651
Fenugreek	(1416)	-----
Guar-GaLT1	(1418)	-----
Guar-GaLT2	(1579)	AAAAAAAAAAAAAAAAAAAAAAACT
Consensus	(1621)	

FIGURE 7c (Sheet 3 of 3)

	1	60
Fenugreek-GaLT	(1) ATKFG-SKN-KSSPWL SNGC ^T FLLGAMS ALL ^M GLNS H ^I APIPNSNPKFN S ^T TKL K ^L SL	
Guar-GaLT1	(1) MAKFG-SRN-KSPKW ISNGCC ^T FLGAFT ALL ^L WGLCS H ^I IP I ^T DPKLN S ^T VATSLRSL	
Guar-GaLT2	(1) MAKSSNSRNKISHVNLS D ^T FLACAFSA F ^I IVWGF S ^T TPN E ^T PESLSVN H ^Q N	
Consensus	(1) MAKFG SRN KS WLSNGC I ^T LLGAFS ALL ^M WGL SFI PIPNS PKFNSL S ^T LKSL	120
	61	
Fenugreek-GaLT	(59) NFTTN-TNFAGP DLLH ^D SDKTFYDDP E ^T CY M ^T MDKPMKN W ^D EKRKEWL H ^F HPSFAAGAR	
Guar-GaLT1	(59) NFPKNPAATL PPNLOH ^D EP T ^T FYDDP E ^T TSY T ^T -MDKPMKN W ^D EKRKEWL H ^L HPSFGAAAR	
Guar-GaLT2	(61) DAVSR--- G ^T D F RF P ^D DR T ^{FYDDPE^MGYT^T-I^DTTVRWDA^KREEWW^RLH^PSFAACAR}	
Consensus	(61) NF SN AGPDL HDPPD K ^T FYDDP E ^T YT MDKPMKN W ^D EKRKEWL HHPSFAAGAR	180
	121	
Fenugreek-GaLT	(118) EKI J ^T TGSQ P ^T KC D ^N P I ^{GDH^LL^LRF^YKN^{KVD^YCR^IHN^DI^TIVYNNALLH^LPKMDSS^TWAKYP}}	
Guar-GaLT1	(118) DKI J ^T TGSQ P ^T KR C ^H N P ^I G D H ^L L ^L R F ^Y K N ^{KVD^YCR^IHN^DI^TIVYNNALLH^LPKMNSS^TWAKYP}	
Guar-GaLT2	(116) ERV J ^T TGSQ P ^T PC R ^N P I ^{GDH^LL^LRF^YKN^{KVD^YCR^IHG^DI^TIVYNNALLH^LPKMFT^TWAKYP}}	
Consensus	(121) EKI J ^T TGSQ P ^T KC NPIGD H ^L L ^L R F ^Y K N ^{KVD^YCR^IHN^DI^TIVYNNALLH^LPKM SYWAKYP}	240
	181	
Fenugreek-GaLT	(178) M V R A AM M H P E V E W I ^T WWVDSDA I ^F TD M B F K ^L PLW R Y K D H N L V I H G W E B I ^T V K T E H S WT G LN	
Guar-GaLT1	(178) M V R A AM M H P E V E W I ^T WWVDSDA I ^F TD M B F K ^L PLIKRYKNHNLV V H G WE G I V R L N H S WT G LN	
Guar-GaLT2	(176) M V R A AM M H P E V E W I ^T WWVDSDA I ^F TD M B V X ^L PLD H Y K D H N L V H G W A H I ^T H K R S WT G LN	
Consensus	(181) M V R A AM M H P E V E W I ^T WWVDSDA I ^F TD M E F K ^L PL RYKDHNLVVHGWE LVK HSWT G LN	300
	241	
Fenugreek-GaLT	(238) AGVFLMRNCQWS I ^D FM D V WAS M GP N S E P Y E K W G ER E R E T F K T V W R D S D Q T A L Y L I A I	
Guar-GaLT1	(238) AGVFLIRNCQWS I ^D FM D V W S MG P Q T E P Y E K W G ER E R E T F K D K ^V T P D S D Q T A L Y L I A I	
Guar-GaLT2	(236) AGVFLIRNCQWS I ^D FM D V W S AS M GP Q T P N Y E K W G Q T L K S T F D K F P E S D D O T G L A Y L I A I	
Consensus	(241) AGVFLIRNCQWS I ^D FM D V WAS M GP Q T P Y E K W G ER L R E T F K D K ^V L P D S D Q T A L Y L I A I	360
	301	
Fenugreek-GaLT	(298) G-EDK W TK K I L M E N E Y Y F E G Y W L E I S K M Y D K G E R I D E J K V W R D S D Q T A L Y L I A I	
Guar-GaLT1	(298) DNKD W REK I F K I L E S E Y Y F E G Y W L E I V K T E N I S M E R V K E A K V S E K Y G A	
Guar-GaLT2	(296) E-K E K W A D K E L E N S E Y Y F E G Y W L E I V G T E N I S K K N E I E T G V R R R H A E K V S E A Y G E	
Consensus	(301) D KDKW DKI L E N E Y Y F E G Y W L E I V K T E N I S E R D E I E K V E G L R R R H A E K V S E K Y G E	420
	361	
Fenugreek-GaLT	(357) M R E E V N K L G --- D M R R P I H F T G C O P C N H H N P I V A --- DD C W N G M E R A L N F A D N Q V L	
Guar-GaLT1	(358) M R E E V N K L D N K --- D R R P I H F T G C O P C N H H N P I V A --- DD C W N G M E R A L N F A D N Q V L	
Guar-GaLT2	(355) E R E E V N K L E A G N G K G S W R R P V I H F T G C O P C N H H N P I V A --- DD C W N G M R K A L N F A D N Q V M	
Consensus	(361) M R E E V N L K D G R R P I H F T G C O P C N H H N P I V A --- DD C W N G M R K A L N F A D N Q V L	451
	421	
Fenugreek-GaLT	(413) K G F I H P N L D K S V S B L F G Y P A S P ---	
Guar-GaLT1	(412) TY G V H R Q N L D K S V S B L F G Y P A ---	
Guar-GaLT2	(415) KY G F V H P D V L D N S V S P I P D V E R N R S G N H I	
Consensus	(421) KY G F I H P N L D K S V S P L P F G Y P A	451

FIGURE 8

		1		60
AtCesA1	(1)	MEASAGLVAGSYRRNELVRIRHESDGG--TKPLKNMNGQICQICGDDVGLAETGDFVAC		
ZmCesA1	(1)	MAANKGMVAGSHNRNEFVMIRHDGDPGSAKPTKSANGQVCQICGDSVGSATGDFVAC		
GhCesA1	(1)	-----MMEGVPVCHTCGEHVGLNVNGEPFVAC		
PtCesa	(1)	-----MMEGAPICHTCGEQVGHDANGELFVAC		
CtMans	(1)	-----		
AtCslA9	(1)	-----		
AtCslB1	(1)	-----		
AtCslC4	(1)	-----		
AtCslD1	(1)	-----MASSPPKKTLNSQSSLSRPPQAVKFGRRTSSGRIVSLSRDDMDVSGDYSQON		
AtCslE1	(1)	-----		
AtCslG1	(1)	-----		
Consensus	(1)	-----		
		61		120
AtCesA1	(59)	NECAFVCRPCYERYERKDGTCQCCPQCKTRFRRHRSRVEGDEDEDDVDDIENEFNYAQG		
ZmCesA1	(61)	NECAFVCRPCYERYERKEGNQCCPQCKTRYKRQKGSRVEHGDEDEEDVDDLDNEFNYKQG		
GhCesA1	(29)	HECNFPICKSCFEYDLKEGRKACLRCGSPY-----D-ENLLDDVEK-ATGDQS		
PtCesa	(29)	HECSYPMCKSCFEFEINEGRKVCLRCGSPY-----D-ENLLDDVEKKGSGNQS		
CtMans	(1)	-----		
AtCslA9	(1)	-----		
AtCslB1	(1)	-----		
AtCslC4	(1)	-----		
AtCslD1	(55)	DYINYTVLMPPTPDNQPAGSSGSTSESKGDANRGGG---GGDGPKMGNKLERRLSVMKS		
AtCslE1	(1)	-----		
AtCslG1	(1)	-----		
Consensus	(61)	-----		
		121		180
AtCesA1	(119)	ANKAR---HQRHGEFFSSSSRRESQP-IPLLTHGHTVSGEIRTPDTQSVRTTSGPLGSPD		
ZmCesA1	(121)	SGKGPEWQLQGDDADLSSSARHEPHRIPRLTSGQQISGEIPDASPDRHSIRS--P---		
GhCesA1	(75)	TMAAHLN---KSQDVGIHARHIS-----S-----VSTLDSEMA-----		
PtCesa	(76)	TMASHLN---DSQDVGIHARHIS-----S-----VSTVDSEMN-----		
CtMans	(1)	-----		
AtCslA9	(1)	-----		
AtCslB1	(1)	-----		
AtCslC4	(1)	-----		
AtCslD1	(111)	NNKSMLLRSQTGDFDHNRWLFE SK-----		
AtCslE1	(1)	-----		
AtCslG1	(1)	-----		
Consensus	(121)	-----		
		181		240
AtCesA1	(175)	RNAISSPYIDPRQPVPVRIVDPSKDLNSYGLGNVDWKERVEGWKLKOEKNMLQMTGKYHE		
ZmCesA1	(175)	---TSSYVDPSPVPVVRIVDPSKDLNSYGLNSVDWKERVESWRVKQDKNMQMVTNKYPE		
GhCesA1	(105)	-----EDN-----GNSIWKNRVESWKEKKKKKKPATTKVER		
PtCesa	(106)	-----DEY-----CNPIWKNRVKSCDKENKKKKRSPKAETE		
CtMans	(1)	-----		
AtCslA9	(1)	-----		
AtCslB1	(1)	-----		
AtCslC4	(1)	-----		
AtCslD1	(135)	-----GKYGIGNAFWSEEDDTYDGGVSKS-----		
AtCslE1	(1)	-----		
AtCslG1	(1)	-----		
Consensus	(181)	-----		
		241		300
AtCesA1	(235)	GKGGEIEGTGSNGEELQMADDTRLPM S RVVPIPSSRL T PYRV V ILRL L ILCFFLQ Y RTT		
ZmCesA1	(231)	ARGGDMEGTGSNGEDMQVDDARLPL S RIVPISSNQLNLYRV V ILRL L ILCFFQ Y RV S		
GhCesA1	(137)	EAEIPPEQQ---MEDKPAPPASQPL S TIIPIPKSRL S APYRTV V IMRL L ILGLFFH Y RV T		
PtCesa	(138)	PAQVPTEQQ---MEEKPSAEASEPL S IVYPIP R NK L TPYRAV V IMRL L ILGLFFH Y RV T		
CtMans	(1)	-----		
AtCslA9	(1)	-----		
AtCslB1	(1)	-----		
AtCslC4	(1)	-----MAPNSVAVTM E KPDNF S LLEINGSDPSSFPDKRK S SPKQFSWFL L KAH		
AtCslD1	(159)	-----DFLDKPKWPL T RVQ I PAK I L S PYR L L V IRL V V V FFF L W W W R IT		
AtCslE1	(1)	-----MVNKDDRIRPVH E ADGEPLFETRRRTGR V IA Y RFFSAS V F V C I CLIWF Y RT G		
AtCslG1	(1)	-----METHRKNSVVGNILH T CHPC R RT I PYRIYA T FHTCG I IALMYHH V H		
Consensus	(241)	D S L YR II I L F YRI		

FIGURE 9a (Sheet 1 of 4)

301 360

AtCesA1 (295) HPVKN --- AYPLWLTSVICEIWFAFSWL LDQFPKWKYPINRETYLDRLAIRYDRDGEP ---
 ZmCesA1 (291) HPVRD --- AYGLWLVSVICEVWFALSWL LDQFPKWKYPINRETYLDRLAIRYDRGEP ---
 GhCesA1 (193) NPVDS --- AFGLWLTSVICEIWFAFSWL LDQFPKWKYPVNRETYIDRLSARYEREGEPE ---
 PtCesa (194) NPVDS --- AFGLWLTSVICEIWFAFSWL LDQFPKWKYPVNRETYIERLSARYEREGEPE ---
 CtMans (1) -----
 AtCslA9 (1) -----
 AtCslB1 (1) ----- MNQ --- NNSVWVVAFLCESFFSFIWILITSIKWSASYKSPERLDERVH -----
 AtCslC4 (51) RLJSC --- LSWLVSSVKKRIAESAKNINEEEDPKSRGKOMYRFIKACLVISSIALS -----
 AtCslD1 (203) NPNEA --- AMWLWGLSIVCEIWFAFSWL LDQFPKWKYPVNRETYIDRLSARYEREGEPE ---
 AtCslE1 (53) EIGDNRTVLDRLIWFMFIVEIWFGLYWWVQTQSSRWNPWWRFPSDRLSRRYR -----
 AtCslG1 (47) SLVTAN --- NTLITCLLSDIVLAFMWATTSRLNPNHRTECPEKYAAKPE -----
 Consensus (301) V LW SVICEIWFAF WL LD PKW PVNR TYIDRLA RYE
 361 420
 AtCesA1 (349) --- SQLVPDVFVSTVDPLKEPPLTANTVLSLSDYDVKYACVSDGSAMLTFESL
 ZmCesA1 (345) --- SQLAPIDMFVSTVDPLKEPPLTANTVLSLSDYDVKYACVSDGSAMLTFESL
 GhCesA1 (247) --- DELAADFVSTVDPLKEPPLTANTVLSLSDYDVKYACVSDGSAMLTFESL
 PtCesa (248) --- SQLAGVDFVSTVDPLKEPPLTANTVLSLSDYDVKYACVSDGSAMLTFESL
 CtMans (1) ----- MRNLIFEPEEGIPGNSSSLRYAWQSIRAPVITPLKLAVIVCSVMSIM
 AtCslA9 (1) ----- MELGDTTSVTPDSFMGYRDDITMQMSMVLQDQIRAPLIVPAIRLGVYICLTMSSV
 AtCslB1 (48) ----- DLPSVDMFVTTADPVREPPILVANTLSSLAVNYPANKLACVSDGCSPLTYFSL
 AtCslC4 (105) --- EIVAHFKKNLDDINRPSWEVYGLVEWSYMAWLSRSRSDYIAPLVISLRSRFTVLF
 AtCslD1 (259) TGRSDLPGVDFVSTADPKEPPLTANTVLSLSDYDVKYACVSDGSAMLTFESL
 AtCslE1 (106) --- SDPLRDLVDFVCTADPVIPEPLLVVNTVLSVTAIDYPPEKIAVYISDDGSELTFYAL
 AtCslG1 (97) ----- DFPLKLDVFTCTADPYKEPPMMVNTALSVMAEYPSDKISVVSDDGSSLTFFAL
 Consensus (361) L VDVFVSTVDPLKEPPLI ANT VLSI LAVDYP DKIS YVSDG A LTF SL
 421 480
 AtCesA1 (406) SETAEFAKKWVPFCKKFNIEPRAPEFYFAQKIDYLKDKIQ -- PSFVKERRAMKREYEEFK
 ZmCesA1 (402) SETAEFKWVPFCKKHNIEPRAPEFYFAQKIDYLKDKIQ -- PSFVKERRAMKREYEEFK
 GhCesA1 (304) VETADFAKWKVPFCKKESIEPRAPEFYFSQKIDYLKDKVQ -- PSFVKERRAMKREYEEFK
 PtCesa (305) VETAEFAKWKVPFCKKESIEPRAPEFYFSQKIDYLKDKVQ -- PSFVKERRAMKREYEEFK
 CtMans (50) LFVERVAMAAVILIVKVLRKKRYTKYNLEAMQKQLERSKK -- YPMVLIQIPMYNEKEVYK
 AtCslA9 (55) LFVERVYMGIVISLVLFGFRKPDKRFKYEPIKDDTELGNSA -- YPMVLIQIPMFNEREVYQ
 AtCslB1 (104) KEASKFAKIWVPFCKKYNIKVRAFPFLNPPAATESS -- EFSKDWETIKREYEEKLS
 AtCslC4 (162) QSLDRLVILCLGCFWIKEKK -- IEPKLTEESIDLEDPSS -- FPMVLIQIPMCNEREVY
 AtCslD1 (319) AEAVRFAEYWVPFCKRKHDIEPRNPDSYFSIKKDPTKNKKR -- QDFVKDRRWIKREYDEEK
 AtCslE1 (163) TEAAEFAKWKVPFCKKFNVEPTSPAAYLSSKANCLDSAEE -- EVAKLYREMAAR -- IETA
 AtCslG1 (153) IEAAKFSKQHPPFCKKNNYQDRSPEVYFSSEHSRSDEAENLKTNTLKCEVEQMMYEDMK
 Consensus (421) E ARFAK WVPFCKKF IE PRAPEFYFS K D L D FVKER MKREYEEFK
 481 540
 AtCesA1 (464) VRINAIKVAKQKIPPEEG ----- WTMQDGTPWPQNN
 ZmCesA1 (460) VRINAIKVAKQKIPPEEG ----- WTMADGTAWPQNN
 GhCesA1 (362) VRINAIKVAKQKTPDEG ----- WTMQDGTPWPQNN
 PtCesa (363) VRINAIKVAKQKTPDEG ----- WTMQDGTPWPQNN
 CtMans (108) LSIGAVCGLSWPADRFI ----- VQLDDSTNP ---
 AtCslA9 (114) LSIGAACGLSWPSDRIV ----- IQVLDDSTDP ---
 AtCslB1 (159) RRVEDATGDSHWLDAED ----- DFEDESNTK
 AtCslC4 (216) OSIGAASQLDWPKDRIL ----- IQVLDDSTDP ---
 AtCslD1 (377) VRINGLPEQIKKRAEQNMREELKEKRIAREKNGVLPDPGVEVVKATWADGTHWPGTW
 AtCslE1 (219) ARLGRIPEEARVKYGDG ----- FSWDADA
 AtCslG1 (213) SRVEHVESGKVETAFIT ----- CDQFRGVFDLWTDKF
 Consensus (481) VRI AL A A E M D T WPG
 541 600
 AtCesA1 (494) TR ----- DHPGMQ - VFLGHSGGLDTDGNE ----- UPRLVVSVREKRPGE
 ZmCesA1 (490) PR ----- DHPGMQ - VFLGHSGGLDTDGNE ----- UPRLVVSVREKRPGE
 GhCesA1 (392) PR ----- DHPGMQ - VFLGYSGARDIEGNE ----- UPRLVVSVREKRPGY
 PtCesa (393) TR ----- DHPGHDGLPWEILGARDIEGNE ----- UPRLVVSVREKRPGY
 CtMans (135) ----- VRELVEMECQKWIQKG ----- V-NVKQENRNRNGY
 AtCslA9 (141) ----- TIKDLVEMECRSWASKG ----- VNIKYEIRDNRNGY
 AtCslB1 (185) PN ----- DHSTIVK - VVWEENKGVGVGN ----- EVPHFVYTSREKRPNY
 AtCslC4 (243) ----- NLQLLIKEEVSVWAEGK ----- V-NITYRHLIRLRTGY
 AtCslD1 (437) FEPKPDHSKGDHAGTQIIMSKVDPLEPVMMGGPNEGALDFTGIDIRVPMFAVSVREKRPGE
 AtCslE1 (244) TRR ----- NHGTILQVLVDGREG ----- N ----- TIAIPTLWVLSREKRPQH
 AtCslG1 (246) SR ----- HDHPTTIIQVLQNSETD ----- MDNTR ----- KYIMPNLTWVSVREKSKVS
 Consensus (541) R DH IIQ L G DG LP LVVSVREKRPGY

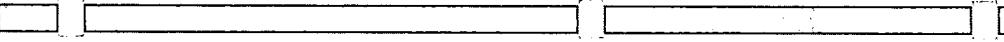
FIGURE 9b (Sheet 2 of 4)

		601		660																				
AtCesA1	(533)	QHHKKACAMNALIRVSAVLTNGAYLLNVPCDHYFNNSKAIKEAMCFMMDPA- ZmCesA1	(529)	QHHKKAGAMNALIRVSAVLTNGAYLLNVCDHYFNSSKAIKEAMCFMMDPA- GhCesA1	(431)	QHHKKAGAENALVRVSAVLTNAPFLILNLDCDHYVNNSKAVREAMCFLMDPQ-VGRDVCYV PtCesa	(433)	QHHKKAGAENALVRVSAVLTNAPYLILNVCDHYVNNSKAVREAMCILMDPQ-VGRDVCYV CtMans	(166)	KAGALKECLEKQY-----VEDCEFVAIFPDAFDQPADFLWNTIPYLLENPK-LGLVQARW AtCslA9	(172)	KAGALKEGMKKSY-----VKSCDYZVAIFPDAFDQPEADFLWRTVPYLLHNPK-LALVQARW AtCslB1	(223)	LHHYKAGAMNFLYRVSGLMTNAPYMLNVDCDMYANEADYVRQAMCIFLQKSMNSNHCAEV AtCslC4	(274)	KAGNLKSAMTCDY-----VKDYEFVTIFPDAFDTPNPDFLKKTPHEKGNPE-LGLVQARW AtCslD1	(497)	DHNKKAGAMNGMVRASAILNSGAFILNLDCDHYIYNSKAIKEGMCFMMDR-GGDRICYI AtCslE1	(281)	HHNFKAGAMNALIRVSSKUTCGKILNLDCDMYANNSKSTRDAICILDEK-EGKEIAFV AtCslG1	(287)	PHHFKAGAINTLIRVSGVMTNSPILTLDCDMYNSNDPFLVRAICVLTDP-EIKSGLGYV Consensus	(601)	HH KAGAMNALVRVSAVLTNG YILNLCD Y N SKAVREAMCFLMDP LG AYV
		661		720																				
AtCesA1	(592)	QFPQRFDGIDLHDRYANRNIFFDINMKGLDGIQGPVYVGTGCCFNQRALYGYDPVLTEE ZmCesA1	(588)	QFPQRFDGIDLHDRYANRNIFFDINMKGLDGIQGPVYVGTGCCFNQRALYGYDPVLTEA GhCesA1	(490)	QFPQRFDGIDRSDRYANRNTVFFDINMKGLDGIQGPVYVGTGCVFNQRALYGYGPPSMPS PtCesa	(492)	QFPQRFDGIDRSDRYANRNVFFDINMKGLDGIQGPVYVGTGCVFNQRALYGYGPPSMPS CtMans	(220)	KFVNSEECMTRLQEMSLDYHFSVEQEVGSSTYAFFGFENGTAGCWRIQAIKDAQ----- AtCslA9	(226)	KFVNNSDECLMTRLQEMSLDYHFTVEQEVGSSTYAFFGFENGTAGCWRIQAIKDAQ----- AtCslB1	(283)	QFPQEF---Y--DSNADELTQLQSYLGRGAGTAGQGPTYAGSCCFHTRRVMYGLS----- AtCslC4	(328)	SEVNKDENMLTRLQNIINLCFHFVEEQVNQGVFLNFFGENTAGCWRIKALEESG----- AtCslD1	(555)	QFPQRFDGIDPSDRYANHNTVFFDGNMRALDGLQGPVYVGTGCMFRRYALYGFNPP--R AtCslE1	(340)	QFPQCFDNVTRNDLYGSMMRVRGIDVFLGLDGNGGPLYIITGCFHRRDVICGRKYG--- AtCslG1	(346)	QFPQKFLGISKNDIYACENKRLFIINMVGFDGIMGPTHVGTGCFNRRAFYGFPP----- Consensus	(661)	QFPQRFDGIDYANN VFFDINMKGLDGIQGPVYVGTGCVF R ALYG
		721		780																				
AtCesA1	(652)	DLEP---NIVKSCCGSRKKKGSSKKYNYEKRRGINRSDSNAPLFNMEDIDEFGEGYDDE ZmCesA1	(648)	DLEP---NIVKSCCGRRKK--KNKSYMDQSRSRIMKRTESSAPIFNMEDIEEGIEGYEDE GhCesA1	(550)	FPK---SSSSSCSCCCCPGKKE---PKDPSELYRDAKREELDAIFNLREIDN--YDEYE PtCesa	(552)	LRKRKDSSSCFSCCCPSKKP---AQDPAEVYRDAKREDLNAIFNLTEIDN--YDEHE CtMans	(274)	-----														
AtCslA9	(280)	-----																						
AtCslB1	(332)	-----		TDDLEDDGSLSLA																				
AtCslC4	(382)	-----																						
AtCslD1	(612)	-----ANEYSGVFGQEKAQAMHVRTQSASQTSQASDLESQDTPQHNDPPDLGLPKKFG																						
AtCslE1	(396)	-----																						
AtCslG1	(400)	-----		YM																				
Consensus	(721)	-----		L D																				
		781		840																				
AtCesA1	(709)	RSILMSQRSVEKREGQSPVFIATFMEQGG-----IPPTTNPATLILKEAIHVISCGYEDK ZmCesA1	(703)	RSVLMQRKLEKREGQSPIFIASTFMTQGG-----IPPTSTNPASLILKEAIHVISCGYEDK GhCesA1	(601)	RSMLISQTSFEKTEGLSSVFIESTLMEENG-----VAESANPSTLILKEAIHVISCGYEK PtCesa	(606)	RSMLISQLSFEKTEGLSSVFIESTLMEENG-----VPESANSPPFIKEAIQVIGCGYEK CtMans	(274)	-----G-----														
AtCslA9	(280)	-----																						
AtCslB1	(346)	TRKYLAEENLAREEGNSNEMVTSVVEALQRK---PNPQNTLANSLEAAQEVGHCHEYQ																						
AtCslC4	(382)	-----		G																				
AtCslD1	(665)	NSTMFTDTIPVAEYQGRPLADHMSVKNGRPPGALLLPRPPLDAPTVAEAIAVISCGYEDN																						
AtCslE1	(396)	-----EEEEEE-----SERIHENLEPEMIKAJASCTYEE																						
AtCslG1	(402)	LILPEIN-ELKPYR-----IADKSIKAQDVISLAHNVAGCIYEN																						
Consensus	(781)	K F		L A V C Y E D																				
		841		900																				
AtCesA1	(764)	TEWGKEIGWYGSVTEDILTCFKMARGIISTYCNPPRPAFKGSAPINLSDRLNQVLRWA ZmCesA1	(758)	TEWGKEIGWYGSVTEDILTCFKMARGWQSTYCMPPRPAFKGSAPINLSDRLNQVLRWA GhCesA1	(656)	TAWGKEIGWYGSVTEDILTCFKMHCRGWSRSTYCMPLRPAFKGSAPINLSDRLHQVLRWA PtCesa	(661)	TEWGKQIGWYGSVTEDILCFKMHCRGWSRSTYCMPPRPAFKGSAPINLSDRLHQVLRWA CtMans	(275)	-----WKDRITVVEDMDLAVRASLHGWFEVFG--DVVKVNELESTFKAYRFQQHRWS AtCslA9	(280)	-----GWKDRITVVEDMDLAVRASLKGWKFYLG--SLVKVNELESTFKAYRYQOHRWS AtCslB1	(402)	TSWGKTIGWYESTAEANTSIGHSRGWTSSYISPCKPAPLFLGAMPPGGP-----MIGORRWA AtCslC4	(383)	-----WLERITVVEDMDLAVRAHNGWKFYLN--DVEVTCELPESYEAYKKQOHRWS AtCslD1	(725)	TEWGDRIGWYGSVTEDVVTGGRMHNRGWRSYCITKRDADFQRTAPINLTDRLHQVLRWA AtCslE1	(427)	TQWGKEMGVKYGPVEDVITGLTICRGWKSAYLNPEKQAFLGVAPTNLHQMLVQORRWS AtCslG1	(441)	TNWGSKIGFRYGSLEVDDYTGMLHCEGWRSSVFCNPKKAAYFYGDSPKCLVDLIVGQQTW Consensus	(841)	T WGKIGWIYGSV EDILTGFKMH RGWRSIYC P R AFKG AP NL D L QQLRWA

FIGURE 9c (Sheet 3 of 4)

		901	902
AtCesA1	(824)	LGSSTEILSRHCPIWYGYHG-RLRRLERLAYINTIVYPITSIPLIAYCILPAFCILITDRF	960
ZmCesA1	(818)	LGSVEILSRHCPIWYGYNG-RLKLLERLAYINTIVYPITSIPLIAYCILPAICLTLNKF	
GhCesA1	(716)	LGSVEIFLSRHCPLWYFGGGRLKWLQLRAYINTIVYPFTSISPLIAYCILPAICLTLGKF	
PtCesa	(721)	LGSVEIFFSRHLPLWYFGGGRLKWLQLRAYINTIVYPFTSISPLIAYCILPAICLTLGKF	
CtMans	(325)	CSPANLIFKMKMTEIICCR-----VPLLKWHHLIYAEFFVRKIVAHWTFFFYCTVIPAC	
AtCslA9	(331)	CGPANLIFRKMAFEIMTNK-----VTLWKKVHVIYSEFFVVRKLVAHIVTFIFCYCILPAT	
AtCslB1	(462)	TGLIEVLFNKQSPUIGMFCR-KIRFRQSLAYIYIFTWGLRSISPELIYCLLPAYCILHNAA	
AtCslC4	(433)	SPPMQLFRLCPLPSIICKSK-----ISVWKKANLIFLEFLRLRKLLIPPEYSFTLFCITPLT	
AtCslD1	(785)	TGSVEIFFSKNNAMFATR-----RLKFLQRVAYINVGIVYPFTSISPLVYVCFLPAICLFSGKF	
AtCslE1	(487)	EGDFOIMLSKYSVSPVWYKGK-----KISLGLLIGCCYCLWAPSSILPVLIYSVLTSLCFLKGIP	
AtCslG1	(501)	VGLFEMFSFSKYSPITYGIKS-----LDLMLGLGCNSPFKPFWSISPLTVYGLLPOALISGV	
Consensus	(901)	G VEIF SKH PIWYG RLKLL LAYIN VYP TSIPLI YC LPALCLT	
	961	962	1020
AtCesA1	(883)	IIPEISNYASIWFILLFISIAVTGILELRLWSGVSTEDWWRNEQFWVIGGTS AHLFAVFGQ	
ZmCesA1	(877)	IIPEISNYAGMFILLFASIATGILELRLWSGVSTEDWWRNEQFWVIGGTS AHLFAVFGQ	
GhCesA1	(776)	IIPTISNLSIATSVLFLGLFISIIVTAVELRLWSGVSTEDLWRNEQFWVIGGVS AHLFAVFGQ	
PtCesa	(781)	IIPTISNLSIATMLFLGLFISIIVTAVELRLWSGVSTEDLWRNEQFWVIGGVS AHLFAVFGQ	
CtMans	(380)	VIVPEVNLNIKKQIATIYDPAITLILNAVTPRSMHLVLWILFENVMSLHRTKAATIGLLE-	
AtCslA9	(386)	VIVPEVTLPKWGAIVTPSIVTLLNAVTPRSMHLVLWILFENVMSLHRTKATFIGLE-	
AtCslB1	(521)	IFP-----KGVLGTVVTLVGMHCLYSLWEMFSLGFSVQSWFASQSFWRKTTGWLFSIPDI	
AtCslC4	(487)	MFPIPEAEIPLWITCIVYPIFISIILNLPKSFSPFIVPVYLLFENTMSITKFNAMISGLFQ-	
AtCslD1	(842)	IVQSLDIHFLSYLCTIVTLLTISLEVWKWSGIGLEENWRNEQFWVIGGTS AHLAAVQG	
AtCslE1	(545)	IFPKVSSSWFIPFGYVITVAAATAYSIAEFLWCGGTRFGWWNEQRMWLYRRTSFLFGMDT	
AtCslG1	(559)	IFPKASDPFWFLWYIILFFGAYAQDLSDFLLEGGTYRKWWNDQRLMLIKGLSFFFQFIEF	
Consensus	(961)	IIP LS L IFI L ISI L LLE WSG SI WW EQFWVI GTSA LFAV Q	
	1021	1022	1080
AtCesA1	(943)	ILKVLAGIDTNFTVTSKATDE-----DGDFEAL-----VIFKWTALLPPPTVIL	
ZmCesA1	(937)	ILKVLAGIDTNFTVTSKASDE-----DGDFEAL-----VIFKWTISLLPPPTVIL	
GhCesA1	(836)	FLKMLAGIDTNFTVTAKAA-----DADEGEL-----VIVKWTITLLEPPPTTLL	
PtCesa	(841)	FLKMLAGIDTNFTVTAKAA-----DAEFGEL-----VMVKWTITLLEPPPTTLL	
CtMans	(439)	---AN-RVNEWWVTEKLG-----NA-----MKQRNNARPS-----	
AtCslA9	(445)	---GCRVNEWIVTEKLG-----	DVKAKSATKT-
AtCslB1	(579)	ILKELGISKTVFIV-----TMPKTMMSGSGSEKSQREVDPCNQDSGKFEFDGSLYFUPGTFIL	
AtCslC4	(546)	FG-SAYEWWVTEKLG-----RS-----SESDLALAFAAKEEK	
AtCslD1	(902)	ILKVIAGIEISFTLTSKASGEDEDDIIFADL-----VIVKWTGLFIMPLTII	
AtCslE1	(605)	IKKILGVSSESAFVITAKVAEEAAERYKEEVMEFG-----VESPMLFLVLTGTLG	
AtCslG1	(619)	ILKTLNLSTPKFNVTSHANDDEQRKRYEQEIFDFG-----TSSSMFLPLTTVA	
Consensus	(1021)	ILKVLAG DT F VTSKAA E F E Y K T L IP TTLL	
	1021	1022	1140
AtCesA1	(987)	IVNLIGIIVAGVSAYAINSGYQSWGPLFGKUUFFALWVIAHLYPFLKGILGRQNR-----	
ZmCesA1	(981)	VINLIVGMVAGISAYAINSGYQSWGPLFGKUUFFSIWVILHLYPFLKGILGRQNR-----	
GhCesA1	(879)	IVNMGVVAAGFSDALNKGYEAWGPLFGKVFFSFVWVILHLYPFLKGILGRQNR-----	
PtCesa	(884)	INMSG-CAGFSDALNKGYEAWGPLFGKVFFAFWVILHLYPFLKGILGRQNL-----	
CtMans	(465)	-----RASRFRIERIH-----	
AtCslA9	(469)	-----S-----K-----KVIRFRFGDRIH-----	
AtCslB1	(639)	IVN-LAAIAGCSVGLQRHGG-GSGLAEACGCCILVVLFLPFLKGILMFEKGK-----	
AtCslC4	(576)	LHRRNS-ESGLLELSKLKEQETNLVQETVKKSLGGMLRPNKKKTNMVF-----	
AtCslD1	(948)	IVNLVAVIAGASRTIYSVIPQWGKLGMGFFFLSLWVILHLYPFLKGILMGRGK-----	
AtCslE1	(653)	MINIFCFAAVARLVSQGDGLDTKMGMFVITGVLLVWINPLYKGMLLRQDK-----G	
AtCslG1	(668)	IVNLVAFWGLYGIIFCG-----GELYLEMLVSEAVNCPLIYGMVLRKDDGKLSKRTC	
Consensus	(1081)	IVNLVG VAG S L G L G WVL LYPF KGLM R	
	1081	1082	1140
AtCesA1	(987)	IVNLIGIIVAGVSAYAINSGYQSWGPLFGKUUFFALWVIAHLYPFLKGILGRQNR-----	
ZmCesA1	(981)	VINLIVGMVAGISAYAINSGYQSWGPLFGKUUFFSIWVILHLYPFLKGILGRQNR-----	
GhCesA1	(879)	IVNMGVVAAGFSDALNKGYEAWGPLFGKVFFSFVWVILHLYPFLKGILGRQNR-----	
PtCesa	(884)	INMSG-CAGFSDALNKGYEAWGPLFGKVFFAFWVILHLYPFLKGILGRQNL-----	
CtMans	(465)	-----RASRFRIERIH-----	
AtCslA9	(469)	-----S-----K-----KVIRFRFGDRIH-----	
AtCslB1	(639)	IVN-LAAIAGCSVGLQRHGG-GSGLAEACGCCILVVLFLPFLKGILMFEKGK-----	
AtCslC4	(576)	LHRRNS-ESGLLELSKLKEQETNLVQETVKKSLGGMLRPNKKKTNMVF-----	
AtCslD1	(948)	IVNLVAVIAGASRTIYSVIPQWGKLGMGFFFLSLWVILHLYPFLKGILMGRGK-----	
AtCslE1	(653)	MINIFCFAAVARLVSQGDGLDTKMGMFVITGVLLVWINPLYKGMLLRQDK-----G	
AtCslG1	(668)	IVNLVAFWGLYGIIFCG-----GELYLEMLVSEAVNCPLIYGMVLRKDDGKLSKRTC	
Consensus	(1081)	IVNLVG VAG S L G L G WVL LYPF KGLM R	
	1141	1142	1192
AtCesA1	(1039)	-TPTIVIVWSVLLASIESLLWVRINPFVANPNANNFNGKGGV-----	
ZmCesA1	(1033)	-TPTIVIVWSVLLASIESLLWVKEDPFTSPTQKAALGQCGVNC-----	
GhCesA1	(931)	-TPTIVIVWSVLLASIESLLWVKEDPFTSPTQKAALGQCGVNC-----	
PtCesa	(935)	-TPTIVIVWSVLLASIESLLWVKEDPFTSPTQKAALGQCGVNC-----	
CtMans	(477)	-PLEIIVGMYMLHCATYDLLFGHDHFFVYLLQAGAFFTMCGFLGVGTIVPT-----	
AtCslA9	(484)	--LELGVMGYUFLVGCDAFEGKHNHYYLFLFAQIAAFFIAGFGQIGTIVPNH	
AtCslB1	(688)	---YGTIPWSTLSKAAEFLAVLFVVFSGN-----	
AtCslC4	(625)	-KKELGIAFLLTAARSFLSAHGLHFYFLFQGLSFLVUGLQLIGEQIS-----	
AtCslD1	(1000)	-VPTIVVWGLVSVITVSLWLWITISPPDDVSGSGISV-----	
AtCslE1	(706)	KMPMSVIVKSVVIALSACTCLAFI-----	
AtCslG1	(724)	FLAGNIVHGSYCVKLLRPPVTSPLRLIHNNTSGWFKRKKHNMMESV-----	
Consensus	(1141)	P IVVVWSVLLAS FSLLW I FV A	

FIGURE 9d (Sheet 4 of 4)

NH₂  **COOH**

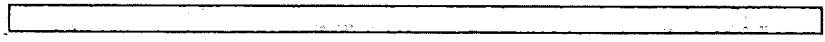
NH₂  **COOH**

FIGURE 10

R S L 10 25 30 E SC Em



FIGURE 11

R S L 10 25 30 E SC Em

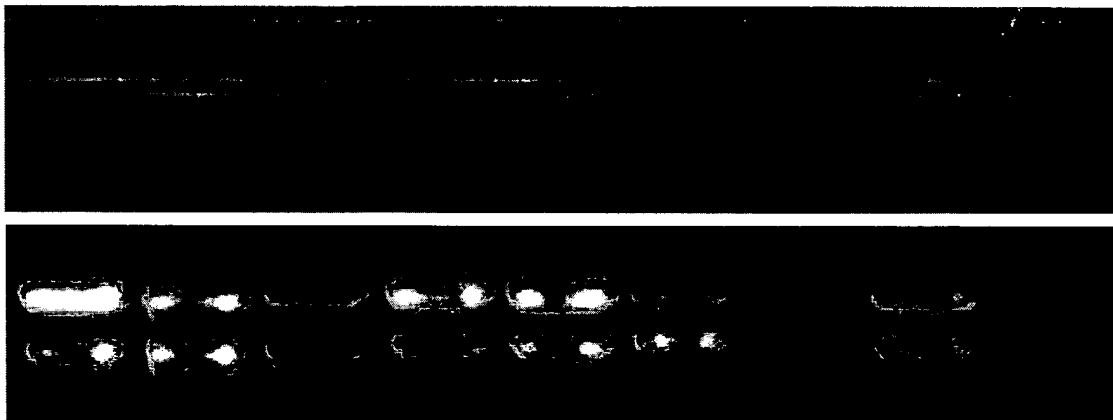


FIGURE 12A

R S L P 10 25 30 40 E SC Em



FIGURE 12B

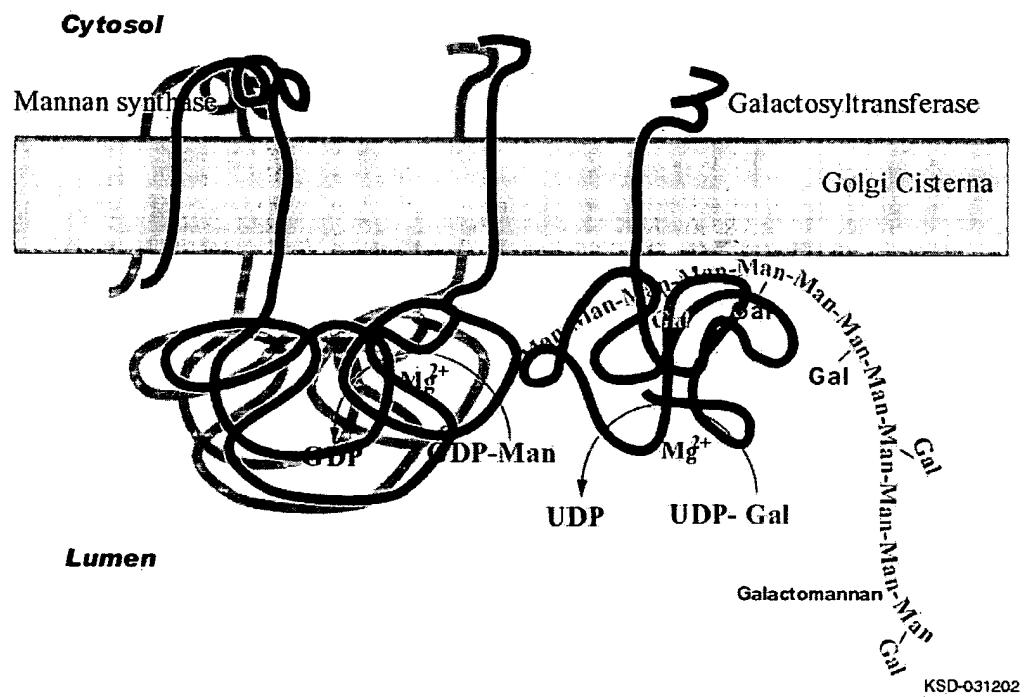


FIGURE 13

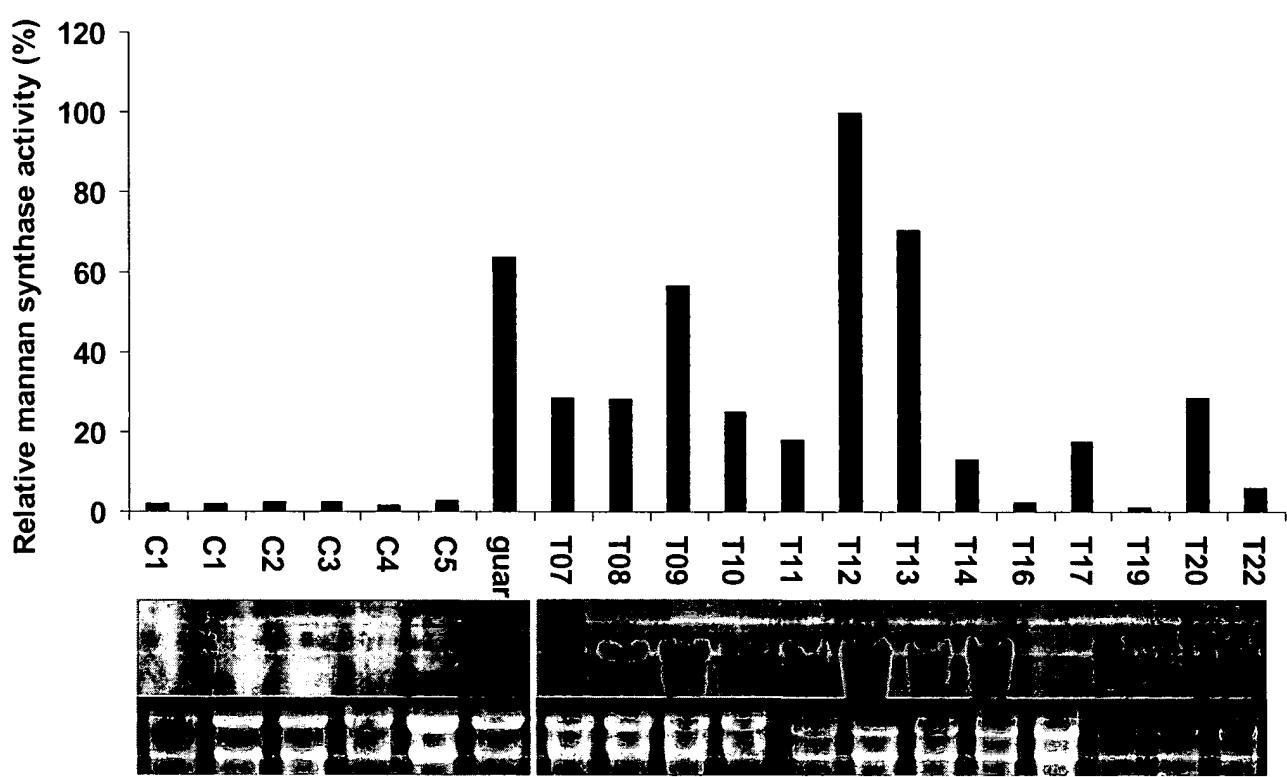


FIGURE 14

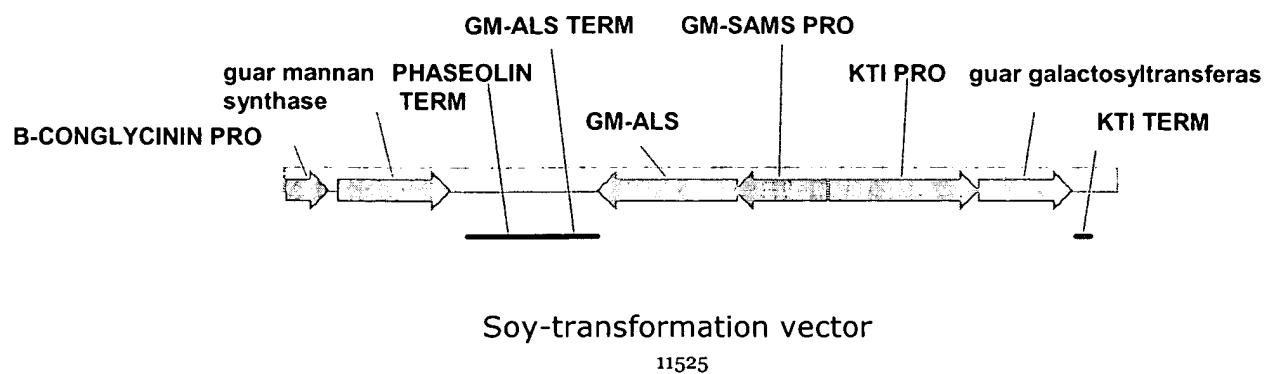


FIGURE 15

1 2 3 4 5 6

β -mannan synthase



α -galactosyltransferase

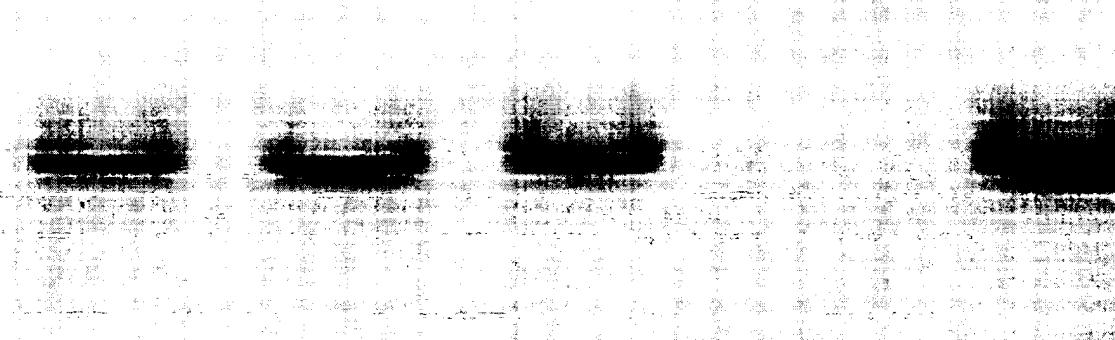


FIGURE 16

A

B

C



FIGURE 17

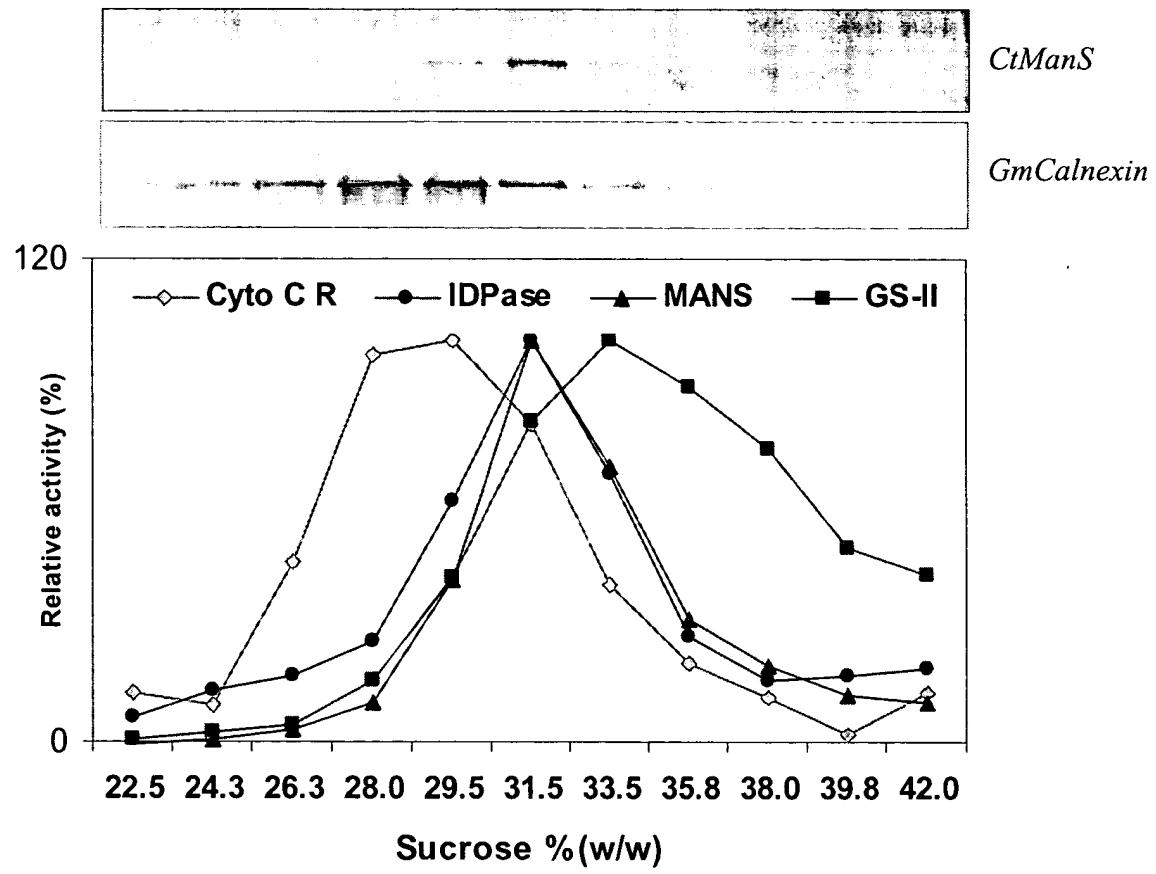


FIGURE 18

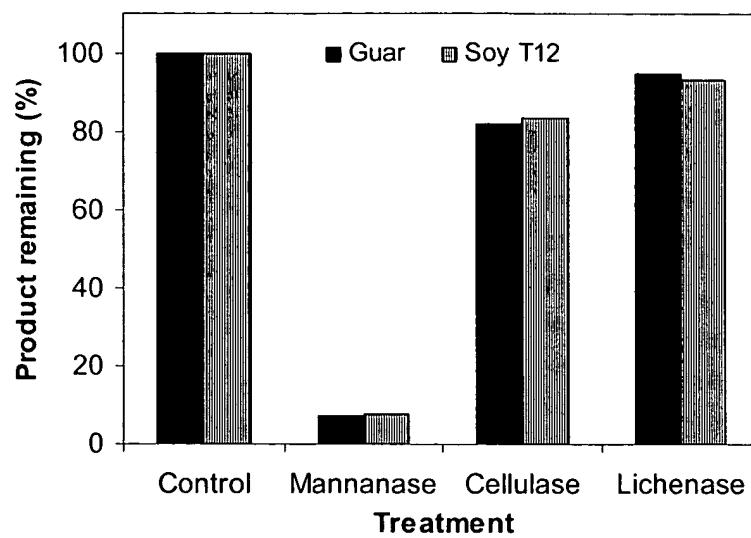


FIGURE 19

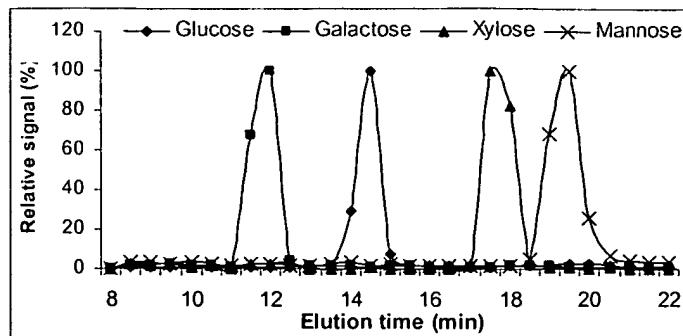


FIGURE 20A

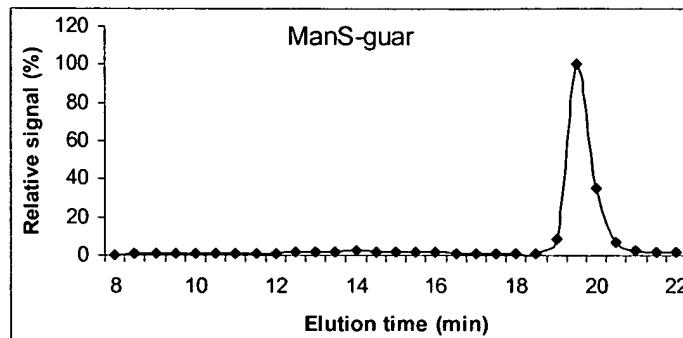


FIGURE 20B

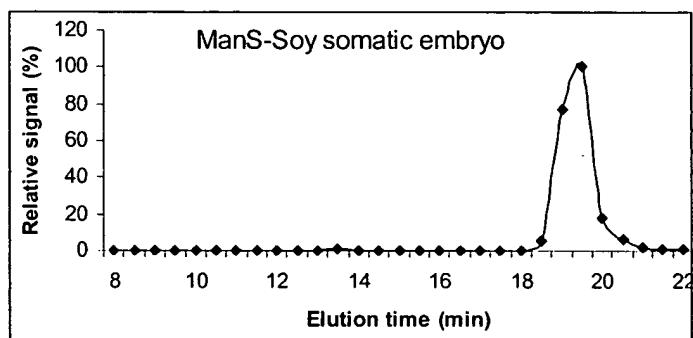


FIGURE 20C

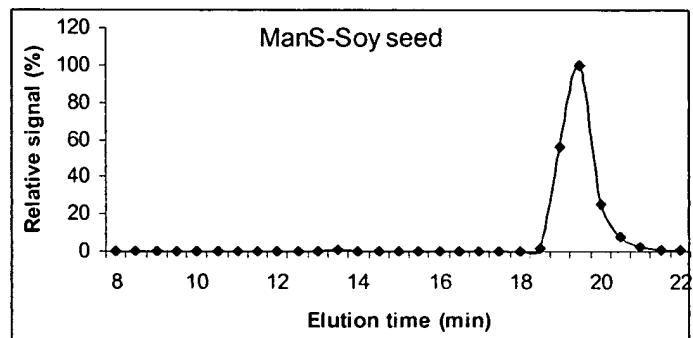


FIGURE 20D

FIGURE 20

>CtGonsT 1349 bp.

GGTGATGCAAATCGCATGAGAGGGAAAGAAGAGGTGTCCTACTTCAATCTTCAT
TCACCCCTTACGAGTGCCACCTCTCTCTCCTCTTCACAGCTCAAACAATTGCTG
TTAAACTTGTGATCGGTTACCATGGAAGAACCTCGTTCCAGTGGAGCGTTATCAG
ATCTCTTGTCCATCCTCAGTGGTGGGTTCAATGTCACCGTTATCGTTAACAA
GTGGATCTCCAGAAATTGGATTCAAGTTCCCTTCAGTATCCTGTGTACACTTAT
CTGCTCAGCAATTGGAGCATATATCGTATTAAGGTGCTGAAGCTAAACCACTGATAAC
TGTTGACCTGATGATCGCTGGAGAAGAAATTTCCTATGTCATTGTATTCTGTATTAA
CATAGTGCCTGGGAATGTGAGCCTACGGTATATCCAGTTCTTTATGCAGACGATAAA
GTCATTACGCCTGCAACTACAGTTGTCATGGCTGTATGGAGAAAGTATTGAA
CTGGCGTATTGGCTCTCTTATTCCATTGGAGGGATTCTCTTACATCTGTAAAC
AGAGCTTAGTTAATATGTTGGATTGTGCTGCCTTATTGGTTGGCACATC
TACGAAGACTATCCTGCAGAATCTCTTGCAATGGGATACAAATTGATAGCATAAACAC
AGTTTACTACATGGCACCCCTTGCAACCATGATCTGGCGCTCCTGCCATGTTACTCGA
AGGAAATGGAATTCTGACTGGCTAAACACTCATCCATATCCTGGTCAGCCCTCATCAT
TATTTTCAGCTCTGGGTTGGCTTCTGTCTCAACTCTCCATTTCACGTGATTCA
CTCCACCACTGCTGTAACCTTAACGTTGCCGGAAACCTTAAGGTTGCAGTTGCTGTTCT
GGTTTCATGGCTGATATTAGGAACCCATATCATACTAAATGCAAGTTGGATGTGCCGT
GACACTTGTGGGATGTACATTCTATGGTTATGTAAGGCACATGCTCTCCAACAGCCACC
AGTTCCAGGAACCTCGAACTCCAAGGACCCCTCGCAGTAAGATGGAGTTACTCCCTCT
TGTAAATGATAAATTAGAAGATAAGGCTAATTGTTAGCTATGTACACGAGGTTATG
TCATTTCTAAGGCAGTAGTAACAGCAATATAGGTACAAAGGATTACAGTGACTGGTTAT
TTATTCCGTTAGATTATCCAAAATTTCAAATACAAGTTCTTACATTCCCTTTAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 21

>CtGONST 0aa, 342 aa.

MEETFVFQWSVIRSLLSILQWWAFNVTVIIVNKWIFQKLDKFPLSVSCVHFICSAIGAY
IVIKVLKLKPLITVDPDDRWRRIFPMSFVFCINIVLGNVSLRYIPVSFMQTIKSFTPATT
VVLQWLVWRKYFDWRIWASLIPIVGGILLTSVTELSFMFGFCAALFGCLATSTKTI
SLLHGYKFDSINTVYYMAPFATMILALPAMLLENGNGILDWLNTHPYPWSALIIIFSSGVL
AFCLNFSIFYVIHSTTAVTFNVAGNLKVAVAVLVSWLIFRNPISYLN
AVGCAVTLVGCTF
YGYVRHMLSQQPPVPGTPRTPRTPRSKMELLPLVNDKLEDKV

FIGURE 22

1	50	
CtGONST	(1)	-----MEETFVFQWSVIR-----
AtGONST5	(1)	-----MEEGSLWROWTMFR-----
AtGONST4	(1)	-----MSSSRFDS-----
AtGONST3	(1)	-----MSTNDEENGTVIEVKN--VPEP--SPE
AtGONST2	(1)	MSAVKLEAIVCHEPDESELSHLSNDNGSKTKNGVVFQLLDQKSSEHRWFSE
AtGONST1	(1)	-----MKLYEH D GVLEDGKT V KSGG---DKP--IPR
Consensus	(1)	MEGS ENGT VIR
	51	100
CtGONST	(14)	-----SLLS I LOWWAFNV T V I IV N WK W IF-----
AtGONST5	(15)	-----SLLS I LOWWGFNV T V I IM N WK W IF-----
AtGONST4	(9)	-----N K QLTTSSLVIGY A ICSSL L AV I NK W AT-----
AtGONST3	(24)	TWYS-----VFLRQASVYGV A AGY C LSASL I SI I NK W AT-----
AtGONST2	(51)	RFLRWRRRYLPVDGDNRRDHGSV K QSGPL V SGAA C SSC S MI I LN K IV L
AtGONST1	(28)	KIH-----NR-----ALLSGL A YC C SSC S MI L VNKFV L
Consensus	(51)	KQ SLLSILAYCISS SLIIINKWII
	101	150
CtGONST	(37)	QKLD F KFPL S VSCVHF I CSAIGAY I V I KV L K I KPL T TVDPDDR R R R IFPM
AtGONST5	(38)	QKLD F KFPL S VSCVHF I CSSIGAY I V I KV L K I KPL T VVD P EDR R R R IFPM
AtGONST4	(37)	TYEN Y PG Y --LLTA Q Y L TCTV A V V Y L LGK S GL I N Y --HD P FTWDTA K K E LP A
AtGONST3	(58)	MKE P Y P Y P --ALTAM Q Y F TS A AGV V LC A Q M KL I E Y --H D SLNLLT M W R EL P PA
AtGONST2	(101)	SSY N FN A GV S SL M LY Y Q M NI S C L V V A V LD I SG V S Y -- Y EKF N WK L IR V W M PV Y
AtGONST1	(56)	SSY N FN A GT I FL M LY Y Q N F V S V I V V G LS M GL I T Y --TEPL T RL M K V W F P V
Consensus	(101)	SKFNF A LSLS VQFI SAIGVYIL KMGLI ID D MRRFFPM
	151	200
CtGONST	(87)	S F V E C I NT I V L GN V S I RY I P V S F M Q T I K S F T P A T T V L Q W L V WR K -Y F D W R
AtGONST5	(88)	S F V E C I NT I V L GN V S I RY I P V S F M Q T I K S S T P A T T V L Q W L V WR K -Y F D W R
AtGONST4	(83)	A I V F Y I A T F T N T N L R H AN D TF I V F RS I T P I V A T A D T Y F RS Q PL P S R L
AtGONST3	(104)	AM I F Y LS I FT N SE L L H AN D TF I V F RS A V P I F V A I G E T L F L H Q P W P S V K
AtGONST2	(149)	N V I F V G ML V SG M Y S LK Y IN V AM V T I KN A T N I L T G I G E V Y M ER K -R Q NN K
AtGONST1	(104)	N V I F V G ML I TS M F S LK Y IN V AM V T I KN V N V I A G E M Y LN K -Q H DN R
Consensus	(151)	AVIF I IVTG SLRYINVA M VIKSLTPILTAIGE LVFRK Y D R
	201	250
CtGONST	(136)	I W ASL T P I V G G I L L T S V TEL S N M F G C A AL F G-----CLAT S T K T I L
AtGONST5	(137)	I W ASL V P I V G G I L L T S V TEL S N M F G C A AL F G-----CLAT S T K T I L
AtGONST4	(133)	T F LSL V V I A G A V GY V A D SS H T I T A Y S W A -----Y L V T T I TEM V Y
AtGONST3	(154)	T W GL A T I F G S L L Y V F D Y Q H T I A A Y S W A -----Y L V S M I ID F V Y
AtGONST2	(198)	V W A A F M M I I S A T SG G I T D L F D AV G Y T W Q LAN C FL T AS S LT I R R V M DK
AtGONST1	(153)	V W A A F L M I I S A V SG G I T D L SE N AV G Y A W Q I A N C FL T AS S LT I R K MT D TD
Consensus	(201)	I W ASL V L I I G G A L L IT D LS F N I GY W A L -----Y L T L ST M I
	251	300
CtGONST	(179)	A E S L H G Y K F D S I NT V Y Y MAP F AT M IL A LP A M L LEG N G I D W L N TH P Y P -
AtGONST5	(180)	A E S L H G Y K F D S I NT V Y Y MAP F AT M IL G LP A F L LE R NG I D W FE A H P SP -
AtGONST4	(176)	I K H M V S N I K L N I W G L V L Y NN L L S LM I A P V F W F L T GE F TE V FA A LS E NR G N
AtGONST3	(197)	I K H V V M T I G I N T W G L V L Y NN L E A L L L F PL E L I MG E L K K I K H E I T D E T -D
AtGONST2	(248)	A K Q S T K G S L N E V SM V L N NN L L S IP F GI T I L I L GE W RY V I S T D V T K D --
AtGONST1	(203)	A K Q V T Q S G N L N E F S SM V L N NN L L S PL G LL S Y F N E MD Y LY Q T P LL R ---
Consensus	(251)	A K LL S K L N S W L V L Y N NN L L A M I G L ALL G E L T

FIGURE 23a (1 of 2)

	301	350
CtGONST	(228) ---WSALIIIFSSGVLAFCLNFSIFYVIHSTTAVTFNVAGNLKVAVALV	
AtGONST5	(229) ---WSALIIILNSGVLAFCLNFSIFYVIQSTTAVTFNVAGNLKVAVALV	
AtGONST4	(226) LFEPYAFSSV A SCVFGFLIS Y FGFAARN A ISATAFTV T CVVNKF T TVVI	
AtGONST3	(246) WYSIQLQVVL P VGLSCLFG A ISFFGFSCRR A ISATGFTV L GIVNK L TVVI	
AtGONST2	(296) ---SMFWVVATASGFLGLAISFTSMWF L HQTGPTTYSLVGSLNK V PI S LA	
AtGONST1	(251) ---PSFW M VM T LSGLLGLAISFTSMWF L HQTGATTYSLVGSLNK T PLS S LA	
Consensus	(301) SAWIIV ASGVGLGLAISFS FW IHATSATTFSVVG LNKIL VLI	
	351	400
CtGONST	(275) SW M IFRNP I SY M NAVGCATLVGCTFY C YVRHMLSQ Q PPVPC G TPRT P RTP	
AtGONST5	(276) SW M IFRNP I SP M NAVCGITLVGCTFY C YVRHMLSQ Q Q - P G TPRT P RTP	
AtGONST4	(276) N M W D KHAT P GLV C ELFT C GGVGYQQ S V K DKPIEKVSEKDSEK G EE	
AtGONST3	(296) N M W D KHST F VG T EL G LCM F GGV M YQ Q ST I K-KP N ATQ E AKPQEQ D EE	
AtGONST2	(343) G L VLFNV P SLPNLFS L FGLFAGV V EARAKMS - - -	
AtGONST1	(298) G L VLFNV P TS L QNSAS L FGLV A GV V EARAKMREKS - - -	
Consensus	(351) LLIF PIS VNAVGL L FTLVGGVVYA AKMM K Q G P	
	401	430
CtGONST	(325) RSKMEL I PLVNDKLEDKV - - -	
AtGONST5	(324) RNK M E L I PLVNDKLES K - - -	
AtGONST4	(326) DE - ELTQLVP G KLASVV - - -	
AtGONST3	(345) QE - KL E EMQENKESNSVDIKETLKSEEKL	
AtGONST2	(376) - - - -	
AtGONST1	(334) - - - -	
Consensus	(401) ELL LV KL V	

FIGURE 23b (2 of 2)

	CtGONST	AtGONST5	AtGONST4	AtGONST3	AtGONST2	AtGONST1
CtGONST	100	90	31	24	16	28
AtGONST5		100	31	22	17	28
AtGONST4			100	51	19	28
AtGONST3				100	17	26
AtGONST2					100	59
AtGONST1						100

FIGURE 24

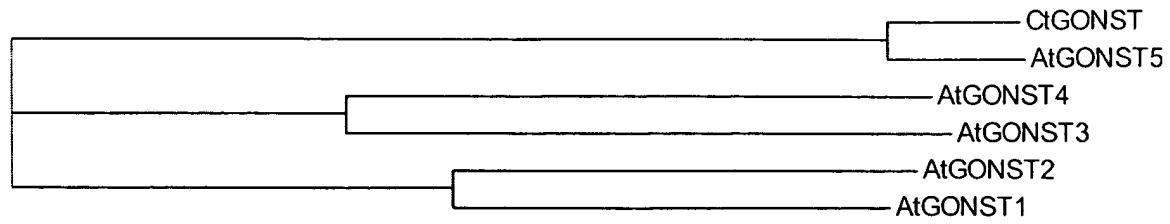


FIGURE 25

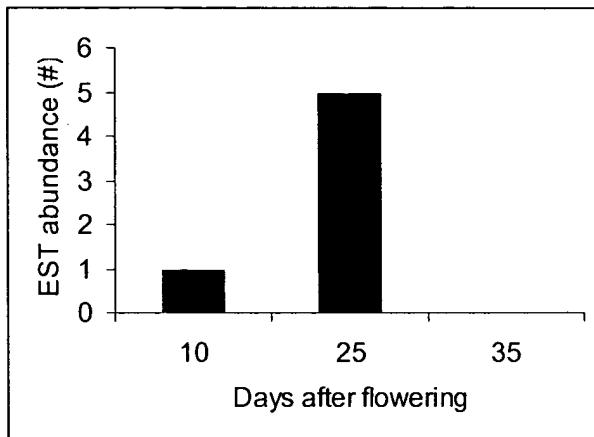
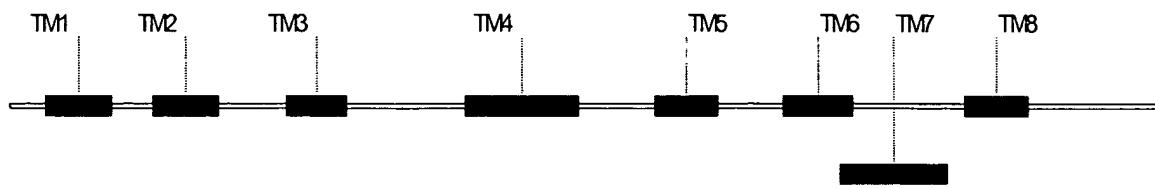


FIGURE 26



CtGONST

342 aa

FIGURE 27